

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: Jun 25, 2003, 14:20:45 ; Search time 5.76512 Seconds
(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613b-26
Perfect score: 606
Sequence: 1 MSNMAFFQCKHIINFTIICN.....ICVCKENQYVHFAGIGRCF 111

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 6
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	96.8	111	1	RNPO_RANCA
2	450	74.3	111	1	LECSLRNJA
3	369	60.9	111	1	RNPL_RANCA
4	272.5	45.0	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANGR_MOUSE
7	135.5	22.4	124	1	RNP_BALAC
8	133.5	22.0	145	1	ANG1_MOUSE
9	132.5	21.9	124	1	RNBR_BOVIN
10	128.5	21.2	151	1	RNBR_CAPCA
11	127.5	21.0	123	1	ANG2_BOVIN
12	127.5	21.0	141	1	RNBR_LARCA
13	127.5	21.0	151	1	RNBR_LARCA
14	126.5	20.9	119	1	RNP_IGUIG
15	126.5	20.9	146	1	ANG1_CERAE
16	126.5	20.9	146	1	ANG1_MIOFA
17	126.5	20.9	146	1	ANG1_SATSC
18	125	20.6	146	1	RNBR_SHEEP
19	123.5	20.4	143	1	RNP_MACRU
20	122.5	20.2	124	1	RNP_MACRU
21	122	19.9	128	1	RNP_MYOCO
22	120.5	19.9	147	1	ANG1_PONPY
23	120.5	19.9	149	1	RNP_MOUSE
24	120.5	19.9	149	1	RNP_MOUSE
25	120	19.8	146	1	ANG1_AOTTR
26	119.5	19.7	143	1	ANG1_PIG
27	118.5	19.6	128	1	RNP_CAVPO
28	118	19.5	146	1	ANG1_SAGOE
29	117.5	19.4	128	1	RNP_HORSE
30	116.5	19.2	124	1	RNP_CANDR
31	116.5	19.2	128	1	RNP_PROGU
32	115.5	19.1	146	1	ANG1_MACMU
33	114	18.8	148	1	ANG1_BOVIN

ALIGNMENTS

RESULT 1	ID	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallid acid-binding lectin) (SBL-C).				
OS	Rana catesbeiana (Bull frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
NCBI_TaxID=8400;					
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-Egg;				
RX	MEDLINE=87299649; PubMed=3304421;				
RA	Tilani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H.,				
RA	Takayanagi G., Hakomori S.;				
RT	"Amino acid sequence of stallid acid binding lectin from frog (Rana				
RT	catesbeiana) eggs.";				
RL	Biochemistry 26:2189-2194(1987).				
RN	[2]				
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.				
RX	MEDLINE=92220613; PubMed=1373237;				
RA	Liao Y.-D.;				
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana				
RT	catesbeiana (bullfrog) oocytes.";				
RL	Nucleic Acids Res. 20:1371-1377(1992).				
RN	[3]				
RP	CHARACTERIZATION.				
RC	TISSUE-Egg;				
RX	MEDLINE=93192604; PubMed=8448385;				
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H.,				
RA	Takayanagi Y., Hakomori S., Tilani K.;				
RT	"Ribonuclease activity of stallid acid-binding lectin from Rana				
RT	catesbeiana eggs.";				
RL	Glycobiology 3:37-45(1993).				
RN	[4]				
RP	STRUCTURE BY NMR.				
RX	MEDLINE=98437383; PubMed=9761686;				
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;				
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes				
RT	of Rana catesbeiana (bullfrog).";				
RL	J. Mol. Biol. 283:231-244(1998).				
CC	-1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE				
CC	RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)				
CC	AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LLECTINS IN FROG EGGS				
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG				
CC	EMBryo. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING				
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND				
CC	HUMAN ORIGIN.				
CC	-1- SUBUNIT: MONOMER.				
CC	-1- SUBCELLULAR LOCATION: Secreted.				
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PIR; A27121; A27121.				

34	113.5	18.7	124	1	RNP_RANCA	P00666 rangifer ta
35	113.5	18.7	125	1	ANG1_RABIT	P31347 oryctolagus
36	113.5	18.7	146	1	ANG1_PAPHA	O8w64 papio hamad
37	113	18.6	147	1	ANG1_HUMAN	P03950 homo sapien
38	113	18.6	147	1	ANG1_PANTR	O8w68 pan troglod
39	112.5	18.6	124	1	RNP_CAPCA	P00664 capreolus c
40	112.5	18.6	124	1	RNP_GIRCA	P00662 giraffa cam
41	112.5	18.6	148	1	RNL4_MOUSE	O9jhl1 mus musculu
42	111.5	18.4	130	1	RNP_CRILLO	P24717 cricetus
43	111.5	18.4	147	1	RNL4_RAT	O55004 rattus norv
44	111.5	18.4	149	1	RNP_ACOCOA	O9wt5 acomys cahi
45	110.5	18.2	124	1	RNP_AEPME	P07847 aepyrocero m

Query Match	Best Local Similarity	96.8%	Score 586.5	DB 1	Length 111
Matches 109	Conservative 0	Mismatches 0	Indels 1	Gaps 1	
DR	PDB: 1BC4: 28-OCr-98.				
DR	InterPro: IP001427: RNaseA.				
DR	Pfam: PF00074: RNaseA; 1.				
DR	ProDom: PD000353: RNaseA; 1.				
DR	SMART: SM00092: RNase_Pc; 1.				
DR	PROSITE: PS00127: RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; Sialic acid; Lactin; 3D-structure.				
FT	MOD_RES	1	1		PYRROLIDONE CARBOXYLIC ACID.
FT	ACT_SITE	10	10		
FT	ACT_SITE	35	35		
FT	ACT_SITE	103	103		
FT	DISULFID	19	71		
FT	DISULFID	34	81		
FT	DISULFID	52	96		
FT	DISULFID	93	110		
SO	SEQUENCE	111 AA: 12464 MW: 0BC9E5F55729ECF4 CRC64:			
QY	3 NMATFQOKHIINTPLII-CNTIMDNIIYVGGQCKRVNFTFIISATYVAICTGVINMVL 61				
Db	2 NMATFQOKHIINTPLIINCNITMDNNIIYVGGQCKRVNFTFIISATYVAICTGVINMVL 61				
QY	62 STTRPOLNTCTRTSTTPRPPCYSSRTETNYICVCKENQYPVHAGIGRCP 111				
Db	62 STTRPOLNTCTRTSTTPRPPCYSSRTETNYICVCKENQYPVHAGIGRCP 111				

FT	DISULFID	94	111
SQ	SEQUENCE	111 AA:	12326 MW; FDEBDDF36834ED679 CRC64;
	Query Match	74.3%;	Score 450; DB 1; Length 111;
	Best Local Similarity	78.2%;	Pred. No. 6,6e-42;
	Matches	86; Conservative	7; Mismatches 15; Indels 2; Gaps 2;
OY	3	NMAAFPOOKHHINTP-IICNTIMDNNIIVYGOCRKRVNFIISATTVAKICTGY-IINNV	60
DB	2	NNAKOEKHIPSTSNINCNTTMDKSTIVYGOCCKERNFIISATTVAKISGVSTNRV	61
OY	61	LSTRFOJLNCRTSITPRPCPYSSRRTENVICVGCENQYVHFAIGIRC	110
DB	62	LSTRFOJLNCRTSATAPRPCPVNSRRTENVICVGCENRLPVHFAIGIRC	111
	RESULT 3		
RNP_L_RANCA	STANDARD:	PRT:	111 AA.
ID	RNP_L_RANCA	STANDARD:	PRT:
AC	P14626;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-FEB-1994 (Rel. 28, last sequence update)		
DT	15-JUN-2002 (Rel. 41, last annotation update)		
DE	Ribonuclease, liver (EC 3.1.27.5).		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
RN	[1]		
RP	NCBI_TaxID=8400;		
RC	SEQUENCE.		
RC	TISSUE=Liver;		
RX	MEDLINE=90130374; PubMed=2613682;		
RA	Nitla R., Katayama N., Okabe Y., Iwana M., Watanabe H., Abe Y.,		
RT	Okazaki T., Ohgi K., Irie M.;		
RT	"Primary structure of a ribonuclease from bullfrog (<i>Rana catesbeiana</i>)		
RL	liver.";		
J.	Biochem. 106:729-735(1989).		
-i-	CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-		
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P		
CC	with 2',3'-cyclic phosphate intermediates.		
-i-	SUBCELLULAR LOCATION: Secreted.		
CC	-i- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	PIR: JX0085; JX0085.		
DR	HSPF, P11916; IBCA.		
DR	InterPro: IPR001427; RNaseA.		
DR	Pfam: PF00074; InaseA; 1.		
DR	Prodom: PD00535; RNaseA; 1.		
DR	SMART: SM00092; RNase_Pc; 1.		
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.		
KM	Hydrolase; Nuclease; Endonuclease.		
FT	MOD_RES	1	PYROLIDONE CARBOXYLIC ACID.
FT	ACT_SITE	10	BY SIMILARITY.
FT	ACT_SITE	35	BY SIMILARITY.
FT	ACT_SITE	104	BY SIMILARITY.
FT	DISULFD	19	BY SIMILARITY.
FT	DISULFD	34	BY SIMILARITY.
FT	DISULFD	52	BY SIMILARITY.
FT	DISULFD	94	BY SIMILARITY.
FT	DISULFD	111	PROBABLE.
SQ	SEQUENCE	111 AA:	DGABAY2456C10788 CRC64;
	Query Match	60.9%;	Score 369; DB 1; Length 111;
	Best Local Similarity	65.5%;	Pred. No. 3,7e-33;
	Matches	72; Conservative	9; Mismatches 27; Indels 2; Gaps 2;
OY	3	NMAFPQOKHHINTPT-CNTIMDNNIIVYGOCRKRVNFIISATTVAKICTGY-IINNV	60
DB	2	NNAKFEKEKHIRSTSIDCNTIMDKAIYIVGCKCKERNFIISSEDNVAIKISGVSPDKE	61
OY	61	LSTRFOJLNCRTSITPRPCPYSSRRTENVICVGCENQYVHFAIGIRC	110
DB	62	LSTRSEKINTCIRDSITPRPCPVHPSPDNNAIVCVCEKOLDPVHFAIGIRC	111

QY	89	TNYICVACENQPVHF	104
Db	123	FRTIICENGMPVHF	138
DT	21-JUL-1986	(Rel. 01, Created)	
DT	21-JUL-1986	(Rel. 01, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).		
OS	Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).		
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;		
OX	NCBI_TaxID=9767;		
RP	SEQUENCE.		
RX	MEDLINE=6277855; PubMed=962870;		
RA	Emmens M., Welling G.W., Beintema J.J.;		
RT	"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic ribonuclease."		
RL	Biochem. J. 157:317-323(1976).		
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- TISSUE SPECIFICITY: PANCREAS.		
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	HSSP: P00656; ISRN.		
DR	InterPro: IPR001427; RnaseA.		
DR	Pfam: PF00074; rnaseA: 1.		
DR	PRINTS: PR00794; RIBONUCLEASE.		
DR	ProDom: PD000535; RIBONUCLEASE: 1.		
DR	SMART: SMO0092; RNase_Pc: 1.		
DR	PROSITE: PS00127; RNASE_PANCREATIC: 1.		
KM	Hydrolase; Nuclease; Endonuclease; Glycoprotein.		
FT	DISULFID 26 84		
FT	DISULFID 40 95		
FT	DISULFID 58 110		
FT	DISULFID 65 72		
FT	ACT_SITE 12 12		
FT	ACT_SITE 41 41		
FT	ACT_SITE 119 119		
FT	CARBOHYD 76 76		
SO	SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;		
Query Match	22.4%	Score 135.5;	DB 1; Length 124;
Best Local Similarity	35.3%	Pred. No. 6.9e-08;	
Matches 39;	Conservative 16;	Mismatches 39;	Indels 23; Gaps
QY	7	FOQKHIT-----NTPICNTIMDNNLNLIYGGCKKRNPFIISSATTYKALICGVINMV	60
Db	8	FORQHMDSGNSGPNPNRYCQNMIMRR-KMGGCKKRPVTFVHESLDDVAVCS--QKNV	63
QY	61	L-----STTFQNLCTRTFTSTTPR-CPYSRTETNYICVAC-NQY-PVHF	104
Db	64	LCKNGRTNCEYSNSTHMTIDCROTGSQSKYPNCAYKTSQKEKHIIIVACEGNPVYVHF	120
RESULT 8			
ID	ANGI_MOUSE	STANDARD;	PRT; 145 AA.
AC	P21570;		
DT	01-MAY-1991	(Rel. 18, Created)	
DT	01-MAY-1991	(Rel. 18, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	

DE Angiogenin precursor (EC 3.1.27.-).
 GN ANG.
 OS Mus musculus (House).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10010;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA."
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RP PARTIAL SEQUENCE.
 RC TISSUE=Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiogenins: discernment of functionally important residues and
 RT regions."
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS. ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAs.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 DR EMBL: U22516; AAA91366.1;
 DR PIR: A35932; A35932.
 DR HSSP: P03950; IAA1;
 DR MGD: MGI:88022; Ang.
 DR InterPro: IPR01427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNase_PANCREATIC.1.
 DR KMW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KM Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 145
 FT MOD_RES 25 25
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 137 137
 FT DISULFID 50 104
 FT DISULFID 63 115
 FT DISULFID 81 130
 SQ SEQUENCE. 145 AA; 16228 MM; 06944260BB764938 CRC64;
 Query Match 22.4%; Score 135.5; DB 1; Length 145;
 Best Local Similarity 39.5%; Pred. No. 8.1e-08;
 Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;
 OY 34 CRRVNFIISSATVAIC--TGVINMV-LSTFRQNTCTRTSTTPR-PCPYSSRTE 88
 Db 63 CKDYVFTHGNKSNKAIKAGNSPYRENLRMSKSPFOVYTTCTHTGSGPRPCQYRASAG 122
 OY 89 TNYVCKENQYVHF 104

Db 123 FRHVIAENGSLPVHF 138
 RESULT 9
 ID RNRB_BOVIN STANDARD; PRT; 167 AA.
 AC P39873;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
 GN BRN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92093604; PubMed=1754384;
 RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
 RA Viola M., Palmieri M., Russo E., Furia A.;
 RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
 RT and its expression in different regions of the brain."
 RL Nucleic Acids Res. 19:6469-6474(1991).
 RN [2]
 RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
 RC TISSUE=Brain;
 RX MEDLINE=89214015; PubMed=3243767;
 RA Matarabe H., Katoh H., Ishii M., Komoda Y., Senda A., Takizawa Y.,
 RA Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bovine brain."
 RL J. Biochem. 104:939-945(1988).
 RN [3]
 RP SEQUENCE OF 27-167 FROM N.A.
 RX MEDLINE=9619017; PubMed=8587129;
 RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
 RA Vento M.T., Furia A.;
 RT "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species."
 RL J. Mol. Evol. 41:850-858(1995).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 CC
 DR EMBL: X59767; CAA2439.1;
 DR PIR: S81744; AAB36138.1;
 DR PIR: S20066; S20066.
 DR PIR: JX0056; JX0056.
 DR HSSP: P00656; 2RNS.
 DR GlycoStDB: P39873;
 DR InterPro: IPR01427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNase_PANCREATIC.1.
 DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 167
 FT ACT_SITE 38 38
 FT ACT_SITE 67 67
 FT ACT_SITE 145 145
 FT DISULFID 52 110
 FT DISULFID 66 121
 FT DISULFID 84 136
 FT DISULFID 91 98
 FT DISULFID 91 98

FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
FT CARBOHYD 155 155 /FTID-CAR_000005.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA: 18450 MW: 681CAAC3CC2FC459 CRC64;
Query Match 22.0%; Score 133.5; DB 1; Length 167;
Best Local Similarity 31.4%; Pred. No. 1.5e-07;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;
OY 5 ATPGKH-----INPIICNTIMDNNTIYVGCGCKRVNFTIISATTVKATCTGYNM 58
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
32 AKFRRHMDSGSSSSSNPNYCNOMMKRR-RMTGRCKPVTNFVHESLDYKAVCS---QK 87
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 59 NVL-----STTRFQLNTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 105
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 88 NITCKNGHPNCYQSKSTMSITDCRETGSSKTPNCAYTSSOKKITTVACGEPVYPVHFD 147
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 106 G 106
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 148 G 148
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
RESULT 10
RNP_PIG STANDARD; PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RN51.
OS Sus scrofa (Pig).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653(1970).
RN [2]
RP REVISION TO 2.
RA Wieringa R.K., Huisinga J.D., Gaastra W., Wellington G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:161-185(1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661(1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00816; NRP.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase: Nuclease: Endonuclease: Glycoprotein.
FT DISULFID 26 84

FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 124 AA: 13804 MW: 0AC28CDE14111845 CRC64;
Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 1.5e-07;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;
OY 7 FQCKHI-----INPIICNTIMDNNTIYVGCGCKRVNFTIISATTVKATCTGYNM 59
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 8 FQROHMDSSSSSNPNYCNLMMSRR-NMTGRCKPVTNFVHESLDYKAVCSQINVCK 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
OY 60 VLSTTRFQLNTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 67 NGQTNQYQNSNTMTITCROTGSSKTPNCAYTKASQEQKHIIIVACGEPVYPVHFD 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
RESULT 11
RNBR_CAPCA STANDARD; PRT; 151 AA.
AC P79351;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS Capreolus capreolus (Roe deer).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Cervoides:
OC Cervidae: Odocoileinae: Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleinedam R.G., Furia A.,
RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC -----
DR EMBL: Y11673; CA72371.1; .
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_PC; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase: Nuclease: Endonuclease: Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA: 16971 MW: 392DDE6302F006A6 CRC64;

